

178363

From: Chernyshev, Olga
Sent: Wednesday, February 01, 2006 2:20 PM
To: STIC-Biotech/ChemLib
Subject: 10/815,297, sequence search request

**Please search SEQ ID NO: 3 down to 60% identity in regular databases only.
Thank you very much!**

Olga N. Chernyshev, Ph.D.
AU 1649
REM 3C89
2-0870
mail 4C70

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 20:47:32 ; Search time 17 Seconds
 (without alignments)
 375.667 Million cell updates/sec

Title: US-10-815-297-3
 Perfect score: 2872

Sequence: 1 MLKQSERRSWSYRPWNTET...KKIAECILGSNPQLTPRQEN 545

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext: 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%)

Maximum Match 100% summaries

Database : Listing first 500 summaries

Published Applications AA New:*

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1: /cgnd_6/prodata/2/pubpaas/US09_NEW_PUB.PEP:*
2: /cgnd_6/prodata/2/pubpaas/US06_NEW_PUB.PEP:*
3: /cgnd_6/prodata/2/pubpaas/US07_NEW_PUB.PEP:*
4: /cgnd_6/prodata/2/pubpaas/PCT_NEW_PUB.PEP:*
5: /cgnd_6/prodata/2/pubpaas/US09_NEW_PUB.PEP:*
6: /cgnd_6/prodata/2/pubpaas/US10_NEW_PUB.PEP:*
7: /cgnd_6/prodata/2/pubpaas/US11_NEW_PUB.PEP:*
8: /cgnd_6/prodata/2/pubpaas/US60_NEW_PUB.PEP:*
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- 6 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
No matches found				

Search completed: February 7, 2006, 20:50:43
 Job time : 17 secs



GenCore version 5.1.7
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OM Protein - protein search, using SW model

Run on:

February 7, 2006, 20:46:31 ; Search time 180 Seconds

(without alignments) 1265.094 Million Cell updates/sec

Title: US-10-815-297-3

Perfect score: 2872

Sequence: I MLKQSERRSWSYRPWNTE.....KKIAECILGSNPQLTPRQEN 545

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqb, 417829326 residues

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%)

Maximum Match 100%)

Listing first 500 summaries

Database : Published Applications AA Min:*

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4: /cgns_6/ptodata/1/pubpaas/us10_PUBCOMB.pep:*

5: /cgns_6/ptodata/1/pubpaas/us10_PUBCOMB.pep:*

6: /cgns_6/ptodata/1/pubpaas/us11_PUBCOMB.pep:*

7: /cgns_6/ptodata/1/pubpaas/us11_PUBCOMB.pep:*

8: /cgns_6/ptodata/1/pubpaas/us12_PUBCOMB.pep:*

9: /cgns_6/ptodata/1/pubpaas/us13_PUBCOMB.pep:*

10: /cgns_6/ptodata/1/pubpaas/us14_PUBCOMB.pep:*

11: /cgns_6/ptodata/1/pubpaas/us15_PUBCOMB.pep:*

12: /cgns_6/ptodata/1/pubpaas/us16_PUBCOMB.pep:*

13: /cgns_6/ptodata/1/pubpaas/us17_PUBCOMB.pep:*

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23: /cgns_6/ptodata/1/pubpaas/us27_PUBCOMB.pep:*

24: /cgns_6/ptodata/1/pubpaas/us28_PUBCOMB.pep:*

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SUMMARIES

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2	2872	100.0	545	3	US-09-918-359-3 Sequence 3, Appli
3	2872	100.0	545	4	US-10-815-227-3 Sequence 4, Appli
4	2862	99.7	545	3	US-09-919-220B-36 Sequence 5, Appli
5	2857	99.5	545	3	US-09-999-220B-116 Sequence 6, Appli
6	2849	99.2	545	3	US-09-999-220B-120 Sequence 7, Appli
7	2803.5	97.6	662	4	US-09-919-220B-24 Sequence 8, Appli
8	2781	96.8	545	3	US-09-999-220B-34 Sequence 9, Appli
9	2778	96.7	545	3	US-09-919-220B-118 Sequence 10, Appli
10	2401	83.6	467	4	US-10-114-270-44 Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-918-359-2
; Sequence 2, Application US 06918359
; Publication No. US0030064490A1
; GENERAL INFORMATION:
; APPLICANT: Wilke, D. Wade
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Priddle, Carl Johan
; APPLICANT: Gerhardt, Brenda
; TITLE OF INVENTION: Novel Human Ion Channel Proteins and Polynucleotides Encoding the

RESULT 2
US-09-833-466-3
; Sequence 3, Application US 09833466
; Publication No. US20040053357A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICager, Inc.
; TITLE OF INVENTION: KY10.1, a No. US20040053357A1 Voltage-Gated Potassium Channel F
; TITLE OF INVENTION: Human Brain
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/833, 466
; CURRENT FILING DATE: 2001-04-11

page
2

PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human alpha subunit
OTHER INFORMATION: channel Kv10.1
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (102)..(514)
OTHER INFORMATION: conserved region of
OTHER INFORMATION: channel Kv10.1
S-09-833-466-3

PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human alpha subunit of voltage-gated potassium
OTHER INFORMATION: channel Kv1.0.1
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (102)..(514)
OTHER INFORMATION: conserved region of voltage-gated potassium
OTHER INFORMATION: channel Kv1.0.1

CURRENT APPLICATION NUMBER: US/10/815,297
CURRENT FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: US/09/833,466
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 3
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human alpha subunit of voltage-gated potassium
OTHER INFORMATION: channel Kv10.1
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1-12) (514)

CURRENT APPLICATION NUMBER: US10/815,297
CURRENT FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: US/09/833,466
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human alpha subunit of voltage-gated potassium
OTHER INFORMATION: channel Kv10.1
FEATURE:
NAME/KEY: PEPTIDE
LOCUTON: (102) (514)

Query Match	Best Local Similarity	Score	DB 3;	Length	545;
Matches	545;	Pred.	No.	5..9e-265;	
	Conservative	0;	Mismatches	0;	Indels
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b	MLKOSERRRSWSYRPNTTENEGSQRSTCSIGARSQSATINGWTGTYNTYIEBEDD	60			
b	MLKOSERRRSWSYRPNTTENEGSQRSTCSIGARSQSATINGWTGTYNTYIEBEDD	60			
b	61 GEEEDQWKDDLAEDQQAGETTAKPEGSDPPALLSTIUVNGHHSYQDYCELAGFPK	120			
b	61 GEEEDQWKDDLAEEQQAGETTAKPEGSDPPALLSTIUVNGHHSYQDYCELAGFPK	120			
b	121 TRIGRLATSTSRSRQLSLCDDYEBOTDEYFDRDAVFPOLVNFYLSGYLVLUDGLCPER	180			
b	121 TRIGRLATSTSRSRQLSLCDDYEBOTDEYFDRDAVFPOLVNFYLSGYLVLUDGLCPER	180			
b	181 FLEELGYWGURLKTPRCCRICPEERRDELSERLKIQHELAQOVAEABLFDRDMRYCG	240			
b	181 FLEELGYWGURLKTPRCCRICPEERRDELSERLKIQHELAQOVAEABLFDRDMRYCG	240			
b	241 PORRLWNLMEKPFRSSVAAKAGIVASSTFLVSVVALLNTVEEMQHQGQEGEGPDRP	300			
b	241 PORRLWNLMEKPFRSSVAAKAGIVASSTFLVSVVALLNTVEEMQHQGQEGEGPDRP	300			
b	301 ILERVEMLMCGFTLEYLRLASTPDRREARSALNLVDVIALPLYQOLLGCFGTGEGH	360			
b	301 ILERVEMLMCGFTLEYLRLASTPDRREARSALNLVDVIALPLYQOLLGCFGTGEGH	360			
b	361 ORGQTVGSVKVGQVLRLVMLMRFLRIKLKLRHSTGLRAFGFTLRCYQVGCLLFTAM	420			
b	361 ORGQTVGSVKVGQVLRLVMLMRFLRIKLKLRHSTGLRAFGFTLRCYQVGCLLFTAM	420			
b	421 GIFTSAAVSVVERDPUSTMFTTIFHSWWMAVSTGSTVSGDMYFETHIGRFAPLCAF	480			
b	421 GIFTSAAVSVVERDPUSTMFTTIFHSWWMAVSTGSTVSGDMYFETHIGRFAPLCAF	480			
b	481 GILNGMPISILYNKFSDYSKLUAYETTIRREGBVNMQARKKKIAECLGSNPQT	540			
b	481 GILNGMPISILYNKFSDYSKLUAYETTIRREGBVNMQARKKKIAECLGSNPQT	540			
b	541 PROEN 545				
b	541 PROEN 545				
b	541 PROEN 545				

; OTHER INFORMATION: conserved region of voltage-gated potassium
; - OTHER INFORMATION: channel Kv10.1
; US-10-815-297-3

ES-10-815-297-3
Sequence 3 Application US11815297
Publication No. US20040157641
GENERAL INFORMATION:
APPLICANT: Jegla, Timothy James
APPLICANT: ICagen, Inc.
TITLE OF INVENTION: Kv10.1, a Novel Voltage-Gated Potassium Channel From Human Brain
FILE REFERENCE: 01851-005910US

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:

February 7, 2006, 20:45:41 ; Search time 51 Seconds

(without alignments)
883.495 Million cell updates/sec

Title: US-10-815-297-3

Perfect score: 2872

Sequence: 1 MLKQSERRSRWSYRPWNTTE KXIAECILGSNPOLTPRQEN 545

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 572060 seqB, 82675679 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 60%
Listing first 500 summaries

Database : Issued Patents AA.*

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3: /cgm2_6/prodata/1/1aa/H_COMB.pep:*
4: /cgm2_6/prodata/1/1aa/PCTUS_COMB.pep:*
5: /cgm2_6/prodata/1/1aa/RG_COMB.pep:*
6: /cgm2_6/prodata/1/1aa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2872	100.0	545	2	US-09-833-466-3

Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-833-466-3

Sequence 3 Application US/09833466

Patent No. 6727353

GENERAL INFORMATION:

APPLICANT: Jegla, Timothy James

APPLICANT: ICagen, Inc.

TITLE OF INVENTION: KV10.1, a No.

TITLE OF INVENTION: Human Brain Voltage-Gated Potassium Channel From

FILE REFERENCE: 018512-005910US

CURRENT APPLICATION NUMBER: US/09-833,466

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: US 60/197,793

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 3

LENGTH: 545

TYPE: PRT

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FEATURE:

OTHER INFORMATION: human alpha subunit of voltage-gated potassium
OTHER INFORMATION: channel Kv10.1
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (102)..(514)
OTHER INFORMATION: conserved region of voltage-gated potassium
OTHER INFORMATION: channel Kv10.1

US-09-833-466-3

Query Match 100.0%; Score 2872; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 4.8e-294;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKQSERRSRWSYRPWNTTE KXIAECILGSNPOLTPRQEN 545
Db 1 MLKQSERRSRWSYRPWNTTE KXIAECILGSNPOLTPRQEN 545

Qy 61 GHEEDWKDIAEEDQOAGETTAKEPREGDPDPAUJSTLUNVNGHSYQDJYCELAGFPK 120
Db 61 GHEEDWKDIAEEDQOAGETTAKEPREGDPDPAUJSTLUNVNGHSYQDJYCELAGFPK 120

Qy 121 TRLGRLATTSRSRQLSLCDQDYEQTDEYTFDRDAVFLQVNFILSVGLVLDGLCP 180
Db 121 TRLGRLATTSRSRQLSLCDQDYEQTDEYTFDRDAVFLQVNFILSVGLVLDGLCP 180

Qy 181 FLEELGYWGVRKYIPRCRICFEERDELSELRIKQHETRAQAQVEAEZELFRDMRFYQ 240
Db 181 FLEELGYWGVRKYIPRCRICFEERDELSELRIKQHETRAQAQVEAEZELFRDMRFYQ 240

Qy 241 PQRRLINLNEKPEFSSVAIGVASTTEVLVSVALLAVTEEMQHQSGESGPDRP 300
Db 241 PQRRLINLNEKPEFSSVAIGVASTTEVLVSVALLAVTEEMQHQSGESGPDRP 300

Qy 301 ILERHEMLCMQFFTYLKLRLASTDPRFARSALNLVDVAILPLQCOLLECTGEH 360
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Qy 361 ORGQTGVSGVKVGQVLVRMULRIFRKILKARHSTGRFTLQCYQQVGCULFIAM 420
Db 361 ORGQTGVSGVKVGQVLVRMULRIFRKILKARHSTGRFTLQCYQQVGCULFIAM 420

Qy 421 GIFTSAVSVHDMPTNFTTISHWWAVSISTVGFGDMYRTHIGRFATLIAF 480
Db 421 GIFTSAVSVHDMPTNFTTISHWWAVSISTVGFGDMYRTHIGRFATLIAF 480

Qy 481 GILNGMPISLYNKEDYISKLUAYETTIRREGEVNPMQRKKAICLGLSNPQLT 540
Db 481 GILNGMPISLYNKEDYISKLUAYETTIRREGEVNPMQRKKAICLGLSNPQLT 540

Qy 541 PROEN 545
Db 541 PROEN 545

Search completed: February 7, 2006, 20:47:16
Job time : 51 secs

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OM protein - protein search, using sw model

Run on: February 7, 2006, 20:38:06 ; Search time 249 Seconds

(without alignments) 1544.229 Million cell updates/sec

Title: US-10-815-297-3

Perfect score: 2872

Sequence: 1 MLKQSERRRSSWSYRPWNTE.....KKIAECLIGSNPQLTPQQEN 545

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%, Maximum Match 100%

Listing first 500 summaries

Database : UniProt 05.80;*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2872	100.0	545	1 KCNV2_HUMAN	08tdn2 homo sapien
2	2872	100.0	545	2 Q8T6X0_HUMAN	05t6x0 homo sapien
3	2302.5	80.2	562	2 Q8cf86_MOUSE	Q8cf86 mus musculus

ALIGNMENTS

RESULT	ID	KCNY2_HUMAN	STANDARD;	PRT;	545 AA.
1	Q8T6X0	KCNV2_HUMAN			
2	Q8cf86	KCNV2_MOUSE			
3	28-FEB-2003	(Rel. 41, Created)			
4	28-FEB-2003	(Rel. 41, Last sequence update)			
5	10-MAY-2005	(Rel. 47, Last annotation update)			
6		potassium voltage-gated channel subfamily V member 2 (voltage-gated potassium channel subunit Kv8.2).			
7		Name=KCNV2;			
8		NUCLEOTIDE SEQUENCE.			
9		Homo sapiens (Human);			
10		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo;			
11		NCBI_TAXID=9606;			
12		TISSUE=Brain;			
13		MEDLINE=2205608; PubMed=12060745; DOI=10.1073/pnas.122617999;			
14		Ottschytach N., Ries A., Van Hoornick D., Snyder D.J.; Obligatory heterotrimerization of three previously uncharacterized Kv channel alpha-subunits identified in the human genome.;			
15		PROC. NATL. ACAD. SCI. U.S.A. 99:7986-7991(2002).			

-!- FUNCTION: Potassium channel subunit. Modulates channel activity by shifting the threshold and the half-maximal activation to more negative values.

-!- SUBUNIT: Heterotrimer with KCNBL1, KCNCl and KCNF1. Does not form homomultimers.

-!- TISSUE SPECIFICITY: Detected in lung, liver, kidney, pancreas, spleen, thymus, prostate, testis, ovary and colon.

-!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.

-!- SIMILARITY: Belongs to the potassium channel family. V subfamily.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use as long as its content is in no way modified and this statement is not removed.

Ensembl; ENSG0000168263; Homo sapiens.

HGNC; HGNC:19688; KCNV2.

MIM: 607604; -

InterPro; IPR005821; Ion_trans.

InterPro; IPR003091; K_channel.

InterPro; IPR001622; K+channel_pore.

InterPro; IPR003131; Kterra.

InterPro; IPR003971; Kv9_channel.

InterPro; IPR003968; Kv_Channel.

InterPro; IPR005820; M+Channel_nlg.

Pfam; PF00520; Ion_trans_1.

Pfam; PF02214; K_tetra_1.

PRINTS; PRO0169; KVCHANNEL.

PRINTS; PRO1494; KVCHANNEL.

KW Glycoprotein; Ion transport; Ionic channel; Multigene family;

KW Potassium; Potassium channel; Potassium transport; Transmembrane;

KW Transport; Voltage-gated channel.

PTP TOPO_DOM 1 155 Cytoplasmic (Potential).

PTP TRANSMEM 156 176 Segment S1 (Potential).

PTP TRANSMEM 262 282 Segment S2 (Potential).

PTP TOPO_DOM 283 336 Cytoplasmic (Potential).

PTP TRANSMEM 337 357 Segment S3 (Potential).

PTP TRANSMEM 375 395 Segment S4 (Potential).

PTP TOPO_DOM 396 410 Cytoplasmic (Potential).

PTP TRANSMEM 411 431 Segment S5 (Potential).

PTP TRANSMEM 472 492 Segment S6 (Potential).

PTP TOPO_DOM 493 545 Cytoplasmic (Potential).

PTP REGION 445 465 Segment H5 (pore-forming) (Potential).

PTP MOTIF 457 462 Selectivity filter (By Similarity).

PTP CARBOHYD 440 440 N-linked (GlycNAc, .) (Potential).

SEQUENCE 545 AA; 62459 MW; 72D175BAC0C6B1DA CRC64;

Query Match 100.0%; Score 2872; DB 1; Length 545; Matches 545; Conservative 0; Misaligned 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 4.7e-219; Mismatches 545; Conservative 0; Misaligned 0; Indels 0; Gaps 0;

QY 1 MLKQSERRRSSWSYRPWNTE.....KKIAECLIGSNPQLTPQQEN 545

Db 1 MLKQSERRRSSWSYRPWNTE.....KKIAECLIGSNPQLTPQQEN 545

QY 61 GREEEDWKDDLABEDQOAGENTAKKEGRSDPPALLSTLNNTNGHSYQDLYCELAGFPK 120

Db 61 GREEEDWKDDLABEDQOAGENTAKKEGRSDPPALLSTLNNTNGHSYQDLYCELAGFPK 120

QY 121 TRGLRATSTSRSQSLCDYEQPEDEYFFDRPAWFQVUNFVLSGVIVLVDLGICPR 180

Db 121 TRGLRATSTSRSQSLCDYEQPEDEYFFDRPAWFQVUNFVLSGVIVLVDLGICPR 180

RL

QY 181 FLEELGYWGRVRLKVTPRCCRCFERRDELRKLQHELAQAOQEAEELFRMRFG 240
 Db 181 FLEELGYWGRVRLKVTPRCCRCFERRDELRKLQHELAQAOQEAEELFRMRFG 240
 QY 241 PORRRLNLMEKPFSSVAAKAGVASSFTPVLYSVVALNTVEEMQHSGCGEGFDLRP 300
 Db 241 PORRRLNLMEKPFSSVAAKAGVASSFTPVLYSVVALNTVEEMQHSGCGEGFDLRP 300
 QY 301 ILEHVELCMGFFTLEYLRLASTPDIRFARSALNVLVAILPJKYQOLLCFCFGEGH 360
 Db 301 ILEHVELCMGFFTLEYLRLASTPDIRFARSALNVLVAILPJKYQOLLCFCFGEGH 360
 QY 361 ORGOTGVSGVKQQLRMLRIFTRIKLARHSTGLRAGFTLRCYQQGCLLFIAM 420
 Db 361 ORGOTGVSGVKQQLRMLRIFTRIKLARHSTGLRAGFTLRCYQQGCLLFIAM 420
 QY 421 GIFTSAAVSVEHDVPUSTNTFTIPHSWWMAVSISVGSDMYPETHLGRRFAFLCAF 480
 Db 421 GIFTSAAVSVEHDVPUSTNTFTIPHSWWMAVSISVGSDMYPETHLGRRFAFLCAF 480
 QY 481 GILNGMPISILYNKFSDYYSKLAKAYETTIRRERGEVNFMQRARKKIAECLGSNPOLT 540
 Db 481 GILNGMPISILYNKFSDYYSKLAKAYETTIRRERGEVNFMQRARKKIAECLGSNPOLT 540
 QY 541 PRQEN 545
 Db 541 PRQEN 545
 PR 541 PRQEN 545
 •

RESULT 2

O5T6X0 HUMAN PRELIMINARY; PRT; 545 AA.
 ID O5T6X0; 05T6X0/7, (Tremblel. 29, Created)
 AC EMBL; AL54723; CAI15124.1; -; Genomic_DNA.
 DT 01-FEB-2005 (Tremblel. 29, Last sequence update)
 DT 01-FEB-2005 (Tremblel. 29, Last annotation update)
 DE Potassium channel, subfamily V, member 2.
 DE Name=KCNV2; OS Homo Sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

Johnson C.; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL54723; CAI15124.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:005245; P:voltage-gated potassium channel complex; IEA.
 DR GO; GO:0005612; P:potassium transport; IEA.
 DR GO; GO:000613; P:potassium ion transport; IEA.
 KW Ion transport; Tonic channel; Transmembrane; Transport.
 SQ SSEQUENCE 545 AA; 62459 MW; 72D1/5B4COC6B1DA CRC64;

Query Match 100.0%; Score 2872; DB 2; Length 545; Best Local Similarity 100.0%; Pred. No. 4; 7e-219; Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIQSERRSWSRPWTNEESQHRSICSGARGSQASIGHWEGNNVYBED 60
 Db 1 MIQSERRSWSRPWTNEESQHRSICSGARGSQASIGHWEGNNVYBED 60
 QY 61 GESEDWKDLDLAEEDQOGEVTAKPGSPDPALLSLTNNVNGHSYOLDCELAGFPK 120
 Db 61 GEEDWKDLDLAEEDQOGEVTAKPGSPDPALLSLTNNVNGHSYOLDCELAGFPK 120
 QY 121 TRIGLATTSRSRQLSCDPEQTDYFPRDPAYFQVNFYLSQGULVLDGLCPRR 180
 Db 121 TRIGLATTSRSRQLSCDPEQTDYFPRDPAYFQVNFYLSQGULVLDGLCPRR 180
 181 FLEELGYWGRVRLKVTPRCCRCFERRDELRKLQHELAQAOQEAEELFRMRFG 240

Db 181 FLEELGYWGRVRLKVTPRCCRCFERRDELRKLQHELAQAOQEAEELFRMRFG 240
 QY 241 PORRRLNLMEKPFSSVAAKAGVASSFTPVLYSVVALNTVEEMQHSGCGEGFDLRP 300
 Db 241 PORRRLNLMEKPFSSVAAKAGVASSFTPVLYSVVALNTVEEMQHSGCGEGFDLRP 300
 QY 301 ILEHVELCMGFFTLEYLRLASTPDIRFARSALNVLVAILPJKYQOLLCFCFGEGH 360
 Db 301 ILEHVELCMGFFTLEYLRLASTPDIRFARSALNVLVAILPJKYQOLLCFCFGEGH 360
 QY 361 ORGOTGVSGVKQQLRMLRIFTRIKLARHSTGLRAGFTLRCYQQGCLLFIAM 420
 Db 361 ORGOTGVSGVKQQLRMLRIFTRIKLARHSTGLRAGFTLRCYQQGCLLFIAM 420
 QY 421 GIFTSAAVSVEHDVPUSTNTFTIPHSWWMAVSISVGSDMYPETHLGRRFAFLCAF 480
 Db 421 GIFTSAAVSVEHDVPUSTNTFTIPHSWWMAVSISVGSDMYPETHLGRRFAFLCAF 480
 QY 481 GILNGMPISILYNKFSDYYSKLAKAYETTIRRERGEVNFMQRARKKIAECLGSNPOLT 540
 Db 481 GILNGMPISILYNKFSDYYSKLAKAYETTIRRERGEVNFMQRARKKIAECLGSNPOLT 540
 QY 541 PRQEN 545
 Db 541 PRQEN 545

RESULT 3

O8CF56 MOUSE PRELIMINARY; PRT; 562 AA.
 ID O8CF56; 08CF56/0, (Tremblel. 23, Created)
 AC DT 01-MAR-2003 (Tremblel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblel. 23, Last annotation update)
 DE Potassium channel, subfamily V, member 2 (Kv1.1 modulatory voltage-dependent potassium channel).
 DE Name=KCNV2; OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

TISSUE=Eye; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RC Strausberg R.L., Feingold E.A., Grouse L.H., Derec J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheimmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.R., Rubin G.N., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Cabaniss T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman J.M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
 RA Schniech A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT and mouse cDNA sequences ", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002);
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RA Stramberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 QY [3]

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OM protein - protein search, using SW model

Run on: February 7, 2006, 20:41:31 ; Search time 45 Seconds
 (without alignments)
 1165.292 Million cell updates/sec

Title: US-10-815-297-3
 Perfect score: 2872
 Sequence: 1 MUKQSERRRWSYRPWNTE.....KKIAECLIGSNPQLTPQQEN 545

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqB, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%
 Maximum Match 100%
 Listing first 500 summaries

Database : PIR_80:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
...

No matches found

Search completed: February 7, 2006, 20:46:19
 Job time : 45 secs

GenCoce version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 20:37:46 ; Search time 197 Seconds

1215.540 Million cell updates/sec

Title: US-10-815-297-3

Perfect score: 2872

Sequence: I MLKQSERRRSWSYRPWNTE.....KKTACELCLGSNPOLTPRQEN 545

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439318781 residues

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 60% ;
Maximum Match 100% ;
Listing First 500 summaries

Database :
A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004as:*
- 9: geneseqp2005as:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2872	100.0	545 5 AAE13610	Aae13610 Human Kv1 Abg10991 Human vol
2	2872	100.0	545 5 AAU75091	Aau75091 Novel hum
3	2872	100.0	545 6 ABP5353	Abp5353 Human Ptot
4	2872	100.0	545 5 AAE13612	Aae13612 Human Kv1 Aae13613 Human Kv1 Aae13614 Human Kv1 Aae13611 Human Kv1 Aae32070 Human TRI
5	2869	99.9	545 5 AAE13613	Aae13613 Human Kv1 Aae13614 Human Kv1 Aae13611 Human Kv1 Aae32070 Human TRI Abg71220 Human K+a
6	2869	99.9	545 5 AAE13614	Aae13613 Human Kv1 Aae13614 Human Kv1 Aae13611 Human Kv1 Aae32070 Human TRI Abg71220 Human K+a
7	2869	99.9	545 5 AAE13611	Aae13613 Human Kv1 Aae13614 Human Kv1 Aae13611 Human Kv1 Aae32070 Human TRI Abg71220 Human K+a
8	2869	99.9	545 5 AAE32070	Aae32070 Human TRI Abg71220 Human K+a
9	2867	99.8	545 6 ABG79220	Abg79220 Human K+a
10	2865	99.8	545 5 AAE75094	Aae75094 Novel hum Abg71239 Human K+a
11	2865	99.8	545 5 AAE75094	Aae75094 Novel hum Abg71239 Human K+a
12	2862	99.7	545 5 ABG79239	Abg79239 Human K+a
13	2862	99.7	545 5 ABG79284	Abg79284 Human K+a
14	2857	99.5	545 5 ABG79286	Abg79286 Human K+a
15	2803.5	97.6	662 5 AAE22925	Aae22925 Human tri
16	2781	96.8	545 5 ABG79238	Abg79238 Human K+a
17	2778	96.7	545 5 ABG79285	Abg79285 Human K+a
18	2661	92.7	801 5 ABP99010	Abb99010 New human
19	2401	83.3	460 6 ABU54563	Abu54563 Human NOV
20	2392.5	83.3	460 8 ABU82027	Abu82027 Human dia
21	2176	75.8	416 5 ABG30989	Abg30989 Human vol

RESULT 1
AAE13610
ID AAE13610 standard; protein; 545 AA.
AC AAE13610;
XX DT 26-FEB-2002 (first entry)
XX DE Human Kv1.1 protein.
XX KW Human; Kv10.1 protein; Kv10 voltage-gated potassium channel;
KW central nervous system disorder; CNS disorder; seizure disorder;
KW Parkinson's disease; migraine; psychotic disorder; Schizophrenia;
KW depression; cognitive disorder; learning disorder; memory disorder;
KW neuropathic pain; vision disorder; prostate hyperplasia; stroke;
KW spermatocyte maturation; infertility; contraceptive agent;
KW neuroprotective agent; gene therapy; vaccine; epilepsy.
XX OS Homo sapiens.
XX PT Key
XX PT Region
XX PT /label S6_domain
XX PT Domain
XX WO200179455-A1.
XX 25-OCT-2001.
XX 13-APR-2001; 2001WO-US012185.
XX 14-APR-2000; 2000US-0197793P.
XX 11-APR-2001; 2001US-00833466.
XX PA (ICAG-) ICAGEN INC.
XX PI Jegla TJ;
XX DR WPI; 2002-026021/03.
XX DR N-PSDB; AAD22817.
PT Kv1.1 polypeptide for identifying potassium channel modulators, comprising an alpha subunit of a Kv10 potassium channel and is capable of forming a potassium channel with voltage-gating characteristics.
PT Claim 16; Fig 1; 81pp; English.
PT The invention relates to human Kv1.1 polypeptides and poly nucleotides. Kv1.1 polypeptides are members of Kv10 subfamily and Kv superfamily or potassium channels. They comprise an alpha subunit of Kv10 potassium channel and are capable of forming potassium channel with voltage-gating characteristic. They are also useful for identifying compounds that increase or decrease ion flux through potassium channels. The identified modulator compounds are useful for treating central nervous system disorders such as epilepsy and other seizure disorders, Parkinson's disease, migraine, psychiatric disorders such as schizophrenia and depression, cognitive disorders such as learning and memory disorders, neuropathic pain, vision disorders, prostate hyperplasia, for controlling spermatocyte maturation and motility, for treating infertility, as contraceptive agents and as neuroprotective agents (e.g. to prevent stroke). Polynucleotides of the invention are useful in gene therapy and vaccines. The present sequence is human Kv10 protein.

QY	1	MKQSERRSYSRPNNTENGSQRSRSISLGARGSGQSISHGTEGNYYIEBEDD	PA (FARB) BAYER AG.
Db	1	MKQSERRSYSRPNNTENGSQRSRSISLGARGSGQSISHGTEGNYYIEBEDD	XX
QY	61	GEEEDQWKKDIAEDQAGENTTAKPEGPSDPALLSTLNNGGHSYQDYLCELAGFPK	XX
Db	61	GEEEDQWKKDIAEDQAGENTTAKPEGPSDPALLSTLNNGGHSYQDYLCELAGFPK	XX
QY	121	TRIGRLATSTSRSQSLCDYEQDYEQFDRPAVOLVNFYLSGVLLVLDGLCPRR	DR WPI: 2002-583653/62.
Db	121	TRIGRLATSTSRSQSLCDYEQDYEQFDRPAVOLVNFYLSGVLLVLDGLCPRR	DR N-PSDB; ABK89197.
QY	181	FLEBLGNGVRLKVTPCCRRCFEEERDELSERLKIQHELRAQAQTEAEELFRDRFYG	XX
Db	181	FLEBLGNGVRLKVTPCCRRCFEEERDELSERLKIQHELRAQAQTEAEELFRDRFYG	XX
QY	241	PQRRLWNLMEKPFFSSVAAKIGVASSTFLVSVVALNTVEEMOHSQCGEGGPDLRP	CC Novel human voltage gated potassium channel protein KV2.2 and polynucleotide, useful for screening modulators that are useful for treating cancer, diabetes, peripheral or central nervous system, and cardiovascular disorders.
Db	241	PQRRLWNLMEKPFFSSVAAKIGVASSTFLVSVVALNTVEEMOHSQCGEGGPDLRP	CC
QY	301	IIEHVNLCMGGFTLLEVLLASTPDRRFAKSALNVLVAILPLVQLLLECFCFGEH	CC
Db	301	IIEHVNLCMGGFTLLEVLLASTPDRRFAKSALNVLVAILPLVQLLLECFCFGEH	CC
QY	361	ORGOTVSVGKGQVRLMRIFRKLRHSTGRAGFTLROCYQQGCLLFIAM	CC
Db	361	ORGOTVSVGKGQVRLMRIFRKLRHSTGRAGFTLROCYQQGCLLFIAM	CC
QY	421	GIFTFSAVSYEHDVSTNFTIPHSWWMAVSISVGIGDMYPERHLGRPAFLCIAF	CC
Db	421	GIFTFSAVSYEHDVSTNFTIPHSWWMAVSISVGIGDMYPERHLGRPAFLCIAF	CC
QY	481	GILNGMPISIILNKFDSDYYSKKAYETTIRBERGVANFNMORARKKIAEELGSNPOLT	CC
Db	481	GILNGMPISIILNKFDSDYYSKKAYETTIRBERGVANFNMORARKKIAEELGSNPOLT	CC
QY	541	PROEN 545	CC
Db	541	PROEN 545	CC
RESULT 2			
ID	ABG3091	Query Match 100.0%; Score 2872; DB 5; Length 545; Best Local Similarity 100.0%; Pred. No. 4-e-291; Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 545 AA:
ID	ABG3091	1 MKQSERRSYSRPNNTENGSQRSRSISLGARGSGQSISHGTEGNYYIEBEDD	
AC	ABG3091;	1 MKQSERRSYSRPNNTENGSQRSRSISLGARGSGQSISHGTEGNYYIEBEDD	
DT	21-OCT-2002 (first entry)	61 GEEEDQWKKDIAEDQAGENTTAKPEGPSDPALLSTLNNGGHSYQDYLCELAGFPK	
DB	XX	61 GEEEDQWKKDIAEDQAGENTTAKPEGPSDPALLSTLNNGGHSYQDYLCELAGFPK	
DB	XX	121 TRIGRLATSTSRSQSLCDYEQDYEQFDRPAVOLVNFYLSGVLLVLDGLCPRR	
DB	XX	121 TRIGRLATSTSRSQSLCDYEQDYEQFDRPAVOLVNFYLSGVLLVLDGLCPRR	
DB	XX	181 FLEBLGNGVRLKVTPCCRRCFEEERDELSERLKIQHELRAQAQTEAEELFRDRFYG	
DB	XX	181 FLEBLGNGVRLKVTPCCRRCFEEERDELSERLKIQHELRAQAQTEAEELFRDRFYG	
DB	XX	241 PQRRLWNLMEKPFFSSVAAKIGVASSTFLVSVVALNTVEEMOHSQCGEGGPDLRP	
DB	XX	241 PQRRLWNLMEKPFFSSVAAKIGVASSTFLVSVVALNTVEEMOHSQCGEGGPDLRP	
DB	XX	301 IIEHVNLCMGGFTLLEVLLASTPDRRFAKSALNVLVAILPLVQLLLECFCFGEH	
DB	XX	301 IIEHVNLCMGGFTLLEVLLASTPDRRFAKSALNVLVAILPLVQLLLECFCFGEH	
DB	XX	361 ORGOTVSVGKGQVRLMRIFRKLRHSTGRAGFTLROCYQQGCLLFIAM	
DB	XX	361 ORGOTVSVGKGQVRLMRIFRKLRHSTGRAGFTLROCYQQGCLLFIAM	
DB	XX	421 GIFTFSAVSYEHDVSTNFTIPHSWWMAVSISVGIGDMYPERHLGRPAFLCIAF	
DB	XX	421 GIFTFSAVSYEHDVSTNFTIPHSWWMAVSISVGIGDMYPERHLGRPAFLCIAF	